

FIGURE 1

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGCAGCCACACCAAGGACTGT
GTTGAAGGGTGTCCCCCTTAAATGTAATACCTCCTCATCTTCTTACACAGTG
TCTGAGAACATTACATTAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA
CTACTCTCTGACAGCTCTAGACTGGTCTTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCCCTGGCTTGTGCTCTGCCAACCCCTCTTAGCCCTCACACATCGCACT
GAAGAACATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTTTCCAACAAGAGAGCCAAGAACCCATTTTTCCA
TTTGATCTGTTCCAATGTGTCCATTGGATGTCAGTGCTATTCACGAGTTGTACATTGCTC
AGATTAGGTTGACCTCAGTCCCAACCAACATTCCATTGATACTCGAATGCTGATCTC
AAAACAATAAAATTAGGAAATCAAAGAAAATGATTTAAAGGACTCACTTCACTTATGGT
CTGATCCTGAACAAACAAGCTAACGAAGATTCACCCAAAAGCCTTCTAACCAACAAAGAA
GTTGCGAAGGCTGTATCTGCCCACAATCAACTAAGTGAATACCACTTAATCTCCAAAT
CATTAGCAGAACTCAGAATTGAAAATAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTGTATAATAATGGGATAGA
GCCAGGGCATTGAAGGGTGACGGTGTCCATATCAGAATTGCGAGAAAAGTGCAC
CAGTTCTAAAGGCTTACCAACTTATTGGAGCTTCACTTAGATTATAATAAAATTCA
ACAGTGGAACTTGAGGATTTAAACGATACAAAGAACTACAAAGGCTGGGCTAGGAAACAA
CAAATCACAGATATCGAAAATGGAGTCTGCTAACATACCACTGAGAGAAATACATT
TGGAAAACAATAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACCTCCAGATA
ATCTTCTTCATTCTAATTCAATTGCAAGAGTGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTATACAGTGCAATAAGTTATTCAACAAACCCGGTGAATACTGGG
AAATGCAACCTGCAACATTCTGTTGAGCAGAATGAGTGTCACTGGAACTTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTAAATATAAGATTCAAAATCCCTACATT
TGGAAACTTGAACTCTTAAATAATGGTAGTATTATATAACAGCAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACCGAATTGCGAACACTATT
GATACATAAGGGTTGAGAGAAACAAGCATCTTGCAGTTCTTGTACAAATGAT
CTTACATAATCTCATGCTTGACCATTCTTCTTCATAACAAAAAGTAAGATATTGGTA
TTAACACTTGTATCAAGCACATTAAAAAGAACTGTACTGAAATGGAATGCTTGACT
TAGCAAAATTGTGCTCTTCATTGCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTGAGATTAACCTGGTAGTACTGTAATATTAAAT
CATCTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGCCCCT
CTTATGTTAAAACAATTCTAAAATAAGCCTCAGTAAATGTCATTACCAACTTGA
TAAATGCTACTCATAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTAATTATT
ACCTGATTTAAAATCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTGCATT
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC
TTCAACTCTAAGGAATATTGGAGATATCCCTTGGAAAGACCTGCTTGGAAAGAGCCTGGA
CACTAACAAATTCTACACCAATTGTCTCTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAACCGAAAGCTCTA
TATAATGCTCAGAGTTCTTATGTATTCTTATTGGCATTCAACATATGAAAATCAGAAA
ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pi: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDSLFPTRPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPEL
KYLQIIFLHSNSIARGVNDFCPTVPKMKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

10730-411650

FIGURE 3

CGGACGCGTGGGCGGACCGTGGGCCCGSGCACCGCCCCCGGCCCTCCGCCCTCCGACTCGCGCCTCC
CTCCCCCTCCGCCGCTCCGCCCTCCTCCCTCCCTCCCTCCGAGCTGTCCTCGCGTCATGCCGAGCCT
CCCCCGGCCGCTGCTGCTCCTCGGGCTGCTGCTCGGCTCCGGCCGGCCGCGCCGGCCAGA
GCCCGCCGCTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCGTTCCGGGAGCCGAGGCTGCACCTTCGGCG
GAAGGTATGCCCTGGACGAGACGTCGGCACCCGACCTAGGGCAGCCATTGGGATGCGCTGCGTGTG
CGCCTGCGAGGCCCTCAGTGGGTGCCGTACCAAGGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACAGA
GTGCCAACCCGGCCTGTGGCAGCCGCGCAGCTGCCGGACACTGCTGCCAGACCTGCCAGCCCCAGAGCGCAG
CAGTCGGAGCGGAGCCGAGCGGCCCTGTCCTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTAGCAGCC
CGGGGAGCCAGGCCGCTGAGGAGCGGGCCGTTGACGCCACACGGACTTCGTCGGCCTGACAGGGCGAG
GTCGAGGCCGCTGGCACGAGCCGAGTCTCGCTGCGCTAGCCTCGCTCTATCTCCTACAGGCCGCT
GGACCGCCCTACCAGGATCCGTTCTCAGACTCCAATGGCAGTGTCTGTTGAGCACCCCTGAGCCCCCACCA
AGATGGCCTGGTCTGTGGGTGTGGCGGGCAGTGCCTCGGTTGTCCTGCGGCTCCTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGGCTGC
AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCTAGGGGATCACCCCTGCTCACTCT
CAGTGCACACAGAGGACTCCTGCACTTTTGCTGCTCTCCGAGGGCTGCTGGAACCCAGGAGTGGGACTAAC
CCAGGTTCCCTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACCTCAGGCAATGTCAGCCCC
GGAACCAGGCTTGCTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGTGGGAGCTGCA
GATGCCCTGGAGTGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT
CCTGCAAAGTGTCTTGCTGGGCTGATGCCCTGATCCAGTCCAGACGGGTGCTGCCGCTCAGCCAGCCTCAC
GCTGCTAGGAAATGGCTCCCTGATCTACAGGTGCAAGTGTAGGGACAAGCAGTGAGGTGGCATGACACT
GGAGACCAAGCCTCAGCGGAGGGATCAGCGACTGTCCTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC
GGCGTGGGTATCTGCCCTGGCTGGGTGCCAGGGCTCATATGCTGCTGCGAGATGAGCTTCTGAAACG
GGGCACCAAGGACTCCCAGACGGAGAGCTCGGGGACCGTGGCTGCCCTGCCCTACTGTGGCATAGCGCCCG
CCATGACACGCTGCCGTGCCCTAGCAGGAGCCCTGGTGTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
CTGGCTTCCCTGGATACCCACTGTCACCTGCACTATGAAGTGCTGCTGGCTGGCTGGCTCAGAACAGG
CACTGTCACTGCCACCTCTGGCTCTGGCAACGCCAGGGCTCGCGCTGCTGAAGGGATTCTATGGCT
AGAGGCCAGGGTGTGGTGAAGGACCTGGAGCGGAAGTGTGCGGCACCTGGAAAAGGCATGGCTCCCTGAT
GATCACCACCAAGGGTAGCCCCAGAGGGAGCTCGAGGGCAGGTGACATAGCCAACCATGTGAGGTGGCG
ACTGCCCTGGAGGCCGGGGCCGAGGGGGTGCAGGGCTGGGATACAGCCTTGCTGCCGCC
TGTGGTGCCTGGTCTCCGCCCTAGGCCGCCAAACCTGGTGTCTGGGCCGGCCAGAACCCACACATG
CTTCTCGAGGGCAGCAGGCCACCGGCCCTGGCTCGCTGGCGCCAAACTACGACCCGCTCTGTCACTCTGCAC
CTGCCAGAGACGAACGGTGTACCTGACCCGGTGTGTGCCACCGGCCAGCTGCCACACCCGGTGCAGGCTCC
CGACCAAGTGTGCCCTGTTGCCCTGAGAAACAAGATGTCAGAGACTTGCAGGGCTGCCAGGAGGCC
AGGAGAGGGCTGCTATTGTGATGGTGACCGAGCTGGCGGGCAGCGGGTACGGTGGCAGCCCGTTGTGCC
CTTGGCTTAATTAAAGTGTGCTGTCACCTGCAAGGGGGACTGGAGAGGTGACTGTGAGAAGGTGCAGTG
TCCCCGGCTGGCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGGTC
GGCCACCCCCAGCTGGGGACCCCATGCAGGCTGATGGGCCCGGGCTGCCCTTGTGAGGGCAGGGTCCC
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCTTGGAGAGATGAGCTGTATCACCTGAGATGTGGGCAGG
GGTGCCTCACTGTGAGCGGGATGACTGTCCTGCACTGTCCTGTGGCTCGGGAAAGGAGAGTCGATGCTGTT
CCGCTGCCAGGCCACCGGCCGGCCAGAGACCAACTGATCCAGAGCTGGAGAAAGAACGCCAGGCTCTTA
GGGAGCAGCCAGAGGGCAAGTGCACCAAGAGGATGGGCCAGCTGGGAAGGGTGGCATCGAGGACCTTCTT
GCATTCTCCTGTGGGAAGGCCAGTGCTTGTCTCTGCTCTGCTGCCCTACTCCACCCACCGACTACCTCTGGGA
CCACAGCTCCACAAGGGGGAGAGGCCAGCTGGGCCAGACCGAGGTGACAGCCACTCCAAGTCTGCCCTGCC
TCGGCTCTGTCTGGAAAGCCCACCCCTTCTCTGTACATAATGTCAGTGCTGTTGGGATTTTAATT
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
TTTTGTATTATTAAACATTCTTTCACTGCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLGLLLGSRPARGAGPEPPVLPIRSEKEPLPVRAAGCTFGGKVYALDE
TWHPDLGQPFGVMRVCVLCAEAPQWGRRTRGPGRVSKNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDHTDFVALLTGPRSQAVAR
ARVSLLRSSLRFSISYRRLDRPTRIRFSDNSGSLFEPAAPTQDGLVCGVWRAPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQGVGGITLLTLSDTED
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQQLLRELQANVSAQEPGFAEVLPNLTQEMD
WLVLGELQMALEWAGRPGRLISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVTAHLLGPPGTGPRRLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLREAAGAEVRALGAPDTASAAPPVV
PGLPALAPAKPGGPGRPRDPNTCFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC
PPSCPHPVQAPDQCCPVCPEKQDVRDLPGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPPF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCKQCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFPEQSWSHPSVPPGEMSCITCRCGAGVPHCERDDCSLPLSCSGKESRCCS
RCTAHRRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCGCCGTCACTGCG
TCCTGGCTCCGGCTCCCGGCCCTCCGGCCGGCC**ATG**CAGCCCCGCCGCCAGCGCCGGTGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTCGAGCGGGGCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG
CCCGGCCCTTGTCTGCGCCGGCGTGCAGCCCTGCCGGAAATGGGGGTGTGCACTCGGCCCTG
AGCCGGACCCGCAGCACCCGGCCCCGCCGGAGGCCTGGCTACAGCTGCACCTGCCCGCCGGGATCTCCGGCG
CCAACTGCCAGCTTGTGAGATCCTTGCCAGCAACCCCTGTCACCATGGCAACTGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTGCAATGAAGGCTATGAAGGTCCAACGTGAAACAGGCACCTCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCGACAGCTTCAGCCTGTTCTGCTACTCAGGAGCCTGACA
AAATCCTGCCCTCGCTCTCAGGCAACGGTACACTGCCTACCTGGCAGCCAAAACAGGGCAGAAAGTTGAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCCCTGTGGAATGCCAGTTAACAGCTCTGCCGGTGGCC
GCCTGGTATCCTTGAAGTGCCACAGAACACCTCAGTCAAGATTGGCAAGATGCCACTGCCTCACTGATTTGC
TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTCAGGCTT
CAGGGGACTGGCTCTGGAGGAGATGCTCGCCTGGGAATAATCACTTATTGGTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTGCGCTTAACCTCTGGTGTGAAGGTCAGCACCTGTGTCGCCGGGGAGAGTCACG
CAAATGACTGGAGTTCAGGAAAAGGAAAATGCACACAGAACGGCTCAGAGGCAACTTTCTGTACCTGTG
AGGAGCAGTACGTGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTGCCAAAACAACCGAGCT
GTATTGATGCAAATGAAAAGCAAGATGGAGCAATTTCACCTGTGTTGCCCTGGTTATACTGGAGAGCTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCCGATCTGCTTGTAAGAAAAGGTGGACCCCTGCCCTCGTCTCCGT
GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTACCTGCAACTGCAGCCCAGGCTTCACAGGGCGA
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCAGCGTGGGACCAGCT
ACAAATGCCCTGTGATCCAGGTACCATGCCCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTCCTGCCAGAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTCGCTAACGTCACTGTCTGAAACGGAGCCACCTGTGACAGCGACGGCCTGA
ATGGCACGTGCATCTGTGACCCGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGAGCTGCCCTGGACAGCCAAATGGTTATAACTGCCACTGCCGATGGTGGGGAG
CAAACGTGAGATCCACCTCCAATGGAAGTCCGGCACATGGCGAGAGCCTCACCAACATGCCACGGACTCCC
TCTACATCATCATTGGAGCCCTCTCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTGCCGCA
TCAGCCGCATTGAATACCAGGGTCTTCCAGGCCAGCCTATGAGGAGTTACAACGTGCCGCAGCATCGACAGCG
AGTTCAGCAATGCCATTGCATCCATCGGCATGCCAGGTTGAAAGAAATCCGGCTGCAATGTATGATGTGA
GCCCATGCCCTATGAAGATTACAGTCCGTGATGACAAACCTGGTCACACTGATTAAGAAACTAAAGATTG**TAAT**
CTTTTTGGATTATTTCAAAAAGATGAGATACTACACTCATTAAATATTTAAGAAAATAAGCTTAA
GAAATTAAAATGCTAGCTCAAGAGTTTCAGTAGAATATTAAGAACTAATTCTGCAAGTTAGTTG
GAAAAAAATATTTAAAACAAAATTGTGAAACCTATAGACGATTTAATGTACCTCAGCTCTAAACTGT
GTGCTCTACTAGTGTGCTTTCACTGTAGACACTATCACGAGACCCAGATTAATTCTGTGGTTGTTACA
GAATAAGTCAATCAAGGAGAAGTTCTGTGTTGACGTTGAGTGCCTGTTCTGAGTAGAGTTAGGAAAACCAC
GTAACGTAGCATATGATGTATAATAGAGTATACCGTTACTAAAAAGAAGTCTGAAATGTTGTTG
AGAAAAGACTAGTTAAATTACTATTCCTAACCGAATGAAATTAGCCTTGCTTATTCTGTGCA
TTATTCTGCACTGTTGTTGAACTTTGTGGAAACATTCTTCAGGTTGTTGTCATTCTGTAACAGTCG
TCGAACTAGGCCTCAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCTGATTGATTA
TTCTTTAAAAGTCAGGGTTCTATATTGTGAGTAAATTAAATTACATTGAGTTGTTG
TAAATGTAAGAGAGTACTGGTCCCTCAGTAGTGAGTATTCTCATAGTGCA
GCTTATTATCTCCAGGATGTT
TTTGTGGCTGTATTGATTGATATGTGCTCTTGCTAATTCCAACCATTGAATAATGTGATC
AAGTCA

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDHQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTESMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGLVLLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTKPSEATFSCTCEEQYVGTFCCEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG
YHGLYCEEYNECLSAPCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPCANVSCLNGATC
DSDGLNGTCICAPGFTGEECDIDINECDSNPCHGGSCLDQPNGYNCHCPHWVGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKKSRAAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGCGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC
AGGAAAAGGAAAATGCACCAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTACCTGTGTTGCCTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGAG

FIGURE 8

CTCTGGAAGGTACGGCCACAGGATTCAAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGTTTCAGGGGACTGGCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAACCT
CTGGTGGTGAAGGTAGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTACACCACGCTGGCGCCCCAGAGCCCACACC**ATGCCGGCACCTAC**
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCTGCAAGAGCAGGCACGGCCCT
GATGCGGGACTTCCCCTCGTGGACGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTCTAGCTACGCCAGACCAGCCTGGAC
AGGCTTAGAGATGCCCTCGTGGCGCCAGTTCTGGTCAGCCTATGCCATGCCAGACCCA
GGACCGGGATGCCCTCGGCCCTCACCCCTGGAGCAGATTGACCTCATGCCGATGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA
GCTCCGCTAACGGCGTCCACTCCTCTACAACAAACATCAGCGGCTGACTGACTTTGGTAG
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGCCCTGGAAGTGTACAGGCACCTGTGATCTCTCCACTCGCTGCC
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTGCCATGGAGTAATACAGTCAACCCATCAGCAAATGT
GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGCCGAAATTCCCTCAGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC
TCGTGGAAACCTGCTCGGGCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCCTGGAGGACAAGTTCCGGATGAGCAGCTGAGCAGTTCCCTGCCACTCCGACCTC
TCACGTCTCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTACTGAGATTCCCATA
CTGGACAGCCAAGTTACCAAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCACCTCCAGTCCTTATTCTGTGGCTCT**GA**
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAATGTTGGACATAG

FIGURE 10

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595.  
<subunit 1 of 1, 433 aa, 1 stop  
<MW: 47787, pI: 6.11, NX(S/T): 5  
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYQ  
QTSLDRLRDGVLGAQFW SAYVPCQTQDRDALRLTLEQIIDLIRRMCA SYSELELVTSAKALND  
TQKLA CLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDA VARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGG DYDGAGKFPQGLE  
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEEWKQS PLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPV LILWL
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N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACCTATAATATTCCGGATTATTACCGTCCCACCATGGGCGCGGATCCGGCGCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTGACCCACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCCTCGTGGACGGCCAC
AACGACCTGCCCTGGTCTAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
CAGATTGACCTCATGCCGCATGTGCTCCTATTCTGAGCTGGAGCTTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTACATGCTGGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCGCTAAGGGCTCCACTCCTTACAA
CAACATCAGCGGGCTGACTGACTTGGTGAGAAGGTGGCAGAAATGAACCGCCTGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGGTGTGCAACAGTGCCTGGAAATGTTCC
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCATGG
GAGTAATACTGCAACCCATCAGCCAATGTGTCCTGTGGCAGATCACTTCGACCACATC
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GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTCCCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACACTGAGATTCCCACACTGGACAGCCAAGTTACAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACTCACACATGCCACCGTGCCAGCACCTGA
ACTCCTGGGGGACCGTCAGTCTCCTCTTCCCCAAAACCCAAGGACACC

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX (S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRCASYSELELVTSAKALND
TQKLAACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVVAEMNRLGMMVDSLHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIIELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLRSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHPDKTHTCPCPAELLGGP
SVFLFPPPKPKDT
```

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC
CTGCGCCACCGCCGCCGAGCCGCAGCCCGCCGCCGCGCCCCCGGCAGCGCCGGCCCC**ATG**CCC
GCCGGCCGCCGGGGCCCCGCCAATCCGCGCGGCCGCCGCGCCGTTGCTGCCCTGCT
GCTGCTGCTCTGCGTCCTCGGGGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA
GACCCACCAAGGAGCCACCGCCGAGGGCCTCTACTGGACCCCTAACGGCGCCGCTGCC
TGAGCTCTCCCGTGTACTCAACGCCCTCACCTGGCTCTGCCCTGCCAACCTCAATGGGT
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATCCTGGCTGGC
TCCTGCCCTCATGTTGGCCTGCCAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTCCTCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTACCA
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGACGTGAGCCCGTGGGGCCTGGAG
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTCAAGGATTCCCTTTCAAGCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCTGAAACCCGGCACCGTGTACTCGTCAAGTGC
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCCTCCACTCCCCCAGTGAGGCCCGGGCCGGCGGGCGTGCACCGC
GGGGCGGAGAGCCGAGCTGGGGCCGGTGCAGCGAGCTCAAGCAGTCCCTGGCTGGCTC
AAGAAGCACCGTACTGCTCCAACCTCAGCTCCGCTCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGACAAGACCCGCAACCAGGACGAGGGATCCTGCCCTGGCAGACGGGCA
CGCGAGAGGTCCGCCAGA**TAAG**CTGTAGGGCTCAGGCCACCCCTCCCTGCCACGTGGAGA
CGCAGAGGCCAACCCAAACTGGGCCACCTCTGTACCCCTACTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCACGT
GAGGCCACCTTGGGTGCACCCAGTGGGTGTTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTAAATAAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

095447489201

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSQARRPPPLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNRRRLPPELSRLVLANSTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTGAHGETFLHTNYSLKYLWRWYQGDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGG
LEDQLSVRWVSPPALKDQLFQAKYQIRYRVEDSDWKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPPSSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

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Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAACCGCTCGCAGCCACAAAGGG**ATGAA**TTCTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGTGCCTACGGTACACTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATGCCATTGTCACTGTGGCTCGGCAG
CTGGACATGTCTCGTCCCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACACTGGCTGCCTACAAATAACTGGAGTCAAAACAATG
TCTGTGTCTAATTCGTAAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTAACACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCA**ATAG**CACCTAGTTCTGAAAACACTGATTACCACTGGCTTAGGTTGATGTCATCTA
ATAGTGCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTACTACCACTTGTCTTAGCCAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTACCTGAAGGCTTGCAA
AATTGTACCATAACCCTTATTAAACATATATTATTGATTGACTTAAATTGTTG
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTAAATAAAA
TGAAGGACTATCTAGTGGTATTCAACATGAATATCATGAACCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATAACCTCACATTCCAATGCCAAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pi: 9.52, NX(S/T): 1

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GACTAGTTCTCTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAAGGACTGGGTGACGGCAGGGCAGGGCGCCTGGCCGGGAGAAGCGCGGGGCTGGAGCACCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGAGGCCGGAGGGGGACTGCGAGAGGACCCGGCTCCGGCTCCGGGTGCCAGCGCTATGAGGCCACTCCTCGTCTGCTGCCCTGGCCTGGCGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCGGGGCACCCGGCTTCCAGGCACGCCGGCCACCATGGCAGCCAGGGCTTGCCGGCGCGATGGCCGACGGCCGACGGCGCGACGGCGCCGGGCTCCGGAGAGAAAGGCAGGGCGGGACCGCGGGGGCCGGGACTGCCGGGACCTCGAGGGACCCCGGGCGAGGAGAGGAGGCCGGACCCCGCGGGCCCACCGGGCTGCCTCCGGCTCTGACGCCAACCTTGCCACCGCGTGCCTGGTGAACAGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCAGGGCTGGGTCTACTACTTGCCGTCCATGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTGAAGAATGGCGAATCCATTGCCCTTTCTTCCAGTTTCGGGGGTGGCCCAAGCCAGGCCCTCGCTCTGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTGCTTAGGCCCACTGCCAAAGTGAGCTCATGCTCTCACTCTAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGGAACAGTGGCTGTGCGATCAGGTCTGGCAGCATGGGCAGTGGCTGGATTCTGCCCAAGACCAAGGAGGTGTGCTGTGCTGGCAAGGAATGGGAACGGGGTGTCTCTCCCTGGTCCTGCTTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGCCCTTTCTCAGAGATCACTCAATAAACCTAAGAACCCCTCATAAAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLLLLGLAAGSPPPLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRGPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQWVQVGVDYIGIYASIKT DSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTG
GCACCACCTGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTCTTGCCTCCTCCCTGCACAACCGCCTGCGCAGCTGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCCTTGTGAAGTGGTCAG
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCGGAGGAGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAACGCTTGTCTGCGCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCCTGGTGTGCTCGCA
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGACCATGCAGGGGGCTCTGTGAGGCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTG
ACGGCCGGTTCCGGGAGGAGGTGCTCGTGTGACATCGGCTACGGGGAGGCCAG
TGTGCCACCAAGGTGCATTTCCCTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAGGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAAGGACATCCTGCCCTCATCTGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATGGGCT
CACCTACAAGACGCCAAGGACTCCTCCGCTGGGCCACAGGGAGCACCGCCTCACCA
GTTTGCCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCCTCAACTGGAACGACCAGCGCTGAAAAC
CCGAAACCGTTACATGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGCCT
GAGGCCTGACCACATGGCTCCCTGCCCTGGGAGCAGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCAGGTTAAGACCACATGCCTCATGTCAAAGAGGTCTCAGA
CCTTGACAAATGCCAGAAGTTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTGTGATTGGGAAGATGGCCTCAATTAGA
TGGCGAAGGGAGAGGACACGCCAGTGGTCAAAAAGGCTGCTCTTCCACCTGGCCAGAC
CCTGTGGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pi: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQQAPMAGALNRKESFLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGACATKVHFPFHTCDLRIDGDC
FMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHI SRWGP GS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACCGCGTGGGCTGGCGCTGCAAAGCGTGTCCCAGCCGGTCCCCGAGCGTCCCCCGCCCGA
CGCCCCGCCATGCTCCTGCTGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGA
GGAAGAGGCGCAGAGCTGGGCCACTCTCGGAGCAGGATGGACTCAGGGTCCGAGGCAAG
TCAGACTGTTGAGAGGCTGAAAACCAAACCTTGTATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCCTTATGCCTTCACTACGGTTCTGCAGAATGCTGAACAGAGCTCTGAAGA
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTCACTACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCAGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCCAGCAAGGACAAGGCCCTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGCAAGTACGAGCACAGCATCAGCGTGCAGCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACACGAGGAGGGCAGTGGCGGGGAAGATGATTCTGGCCTCCCCCAT
CTACTGTCACTAACCAAAATGAAACATTGCCAACATAATTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAGAATGAAATTGGAGACTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGACATCCAGTTCTAAATGGCTATTGTGCACTACTTGCTCCTA
AAGACCTCCTCCTTACCCAGAATGTGGTATTGTGCTGACAGCAGTGTCTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTCACAAATTCTCATGACCTCCGACCCCA
GGACCGTTCACTATGGATTTCACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGTACATTACCATATGTCACCCACTGGG
GGCACAGACATCAACGGGCCCTGCAGAGGGCCATCAGGCTCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACGGAGCGTGTCCCTCATCGTCTTGTACGGATGGGAAGGCCACGG
TCGGGGAGACGCACACCTCAAGATCTCAACAAACACCCAGAGGGCCGGAGGCCAAGTC
TGCATCTCACCATTGGCATGGCAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTGCT
GGAGAACTGTGGCCTCACACGGCGTGCACGAGGAGGAGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCGCTCCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCAACTACTTCAACGGCTCGAGATCATCAT
TGCAGGGAAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCTCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGAAAGAT
GTCACAGGAAGCCCCAGGCCTGGAGGGCATGGAGAGGGGACACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGAACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCAGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTGCTCAAGAAGCCAAACTCCGTAAAAAAACAAAAACAAACAAAAAGA
CATGGGAGAGATGGTGTGTTCTCCACACCTGGGATAACGATGAGAAGATGCCACCT
GCAAGCCAGGAAGACGCCCTCACCAGACACCAGTGTCTGCTGGCACCTTGATCTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, PI: 9.54, NX(S/T): 6

MLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLKTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE
KRNKTTEENGEGTEIFRASAVIPSKDKAAFFLSYEELLQRLGKYEHSISVRPQQLSGRSL
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGT
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIIAAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTG
SPRPGGDGEGETNHIERLWSYLTTEKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGCGCGCGCGCCTCCCGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGG
CACTGATCCCCACAGGTGATGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGG
GAGGTTGCGACCATCAGTGCAAGTCAATAAGAGTGACGACTCTGTGATTGACTACTGAA
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGCAGCAGGTTCACT
TGCTGAATTTCTAGCAGTGAACCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACATCACAGT
CCTGGTCCCACCGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGCCAGCAAGCCAGCAGACTATCAGGTGGTCAAA
GGGAACACAGAGCTAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGACAAGGAGGACATGGGTCCCAGTGATCTGCCAGGTGG
AGCACCCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACCTGGTGAGAGTCGATG
ATGAAATGCCAACACGCCGTACTGTCTGGGCCAACCTGTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTCAAACATAGTGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACATCCCTCCTCCCACAACAACCACCA
CCACCACCACCACCACCATCCTTACCATCATCACAGATTCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGTGGCGTGTGGCGGTGGTGGTGGTGGTGG
GCTGTGCTTGCTCATCATTCTGGGCGCTATTTGCCAGACATAAAGGTACATACTCACTC
ATGAAGCAAAGGAGCCGATGACCCAGCAGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCTTTGTGTTCAAT
GAGGTGTCCAACTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

09544747-09544747-09544747-09544747-09544747

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, PI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAAPPGLLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKG
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCCCGA
CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTC
CCGGGACAGAAGA**T**GTGCTCCAGGGCTCCCTGTGCTGCGCTGCTCTGCTACTGCCCT
GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGAGCCAGCACAGACAGTCTTCT
GCACTGCCGCCAGGGACACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC
GTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCTTGCCGCCCTGCCGGCTGCA
GCTCCTGGACCTGTCACAGAACCAAGATGCCAGCCTGCCCTGCCCTGCCCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGCCCTGGAGGCCAGCATTGGACACTGCCAACGTGGAG
GCGCTGCCGCTGGCTGGTCTGGGCTGCAGCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
CAACCTCCACGACCTGGATGTGTCAGAACCCAGCTGGAGCGAGTGCAGCTGCCAGCTGCC
GCCTCCGGGCTGACGCCCTGCCGCTGGCCAGAACACCCGATTGCCAGCTGCC
GAGGACCTGCCGCCCTGCCCTGCAGGAGCTGGATGTGAGAACCTAACGCCCTGCC
CCTGCCTGGCGACCTCTGCCCTCTTCCCCGCCCTGCCGCTGCTGCCAGCTGCCGCC
CCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTGGGTGCGCGAGAGCCACGTCACA
CTGCCAGCCCTGAGGAGACGCCACTTCCGCCAACAACGCTGCCGGCTGCTCCT
GGAGCTTGAACCGCCACTTGGCTGCCAGCCACCAACACCAGCCACAGTGCCACCA
CGAGGCCCGTGGTGCAGGCCACAGCCTGTCTAGCTTGGCTCCTACCTGGCTTAGC
CCCACAGCGCCGCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCC
TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTAATGGGGCACATGCCACCTGG
GGACACGGCACCACTGGCGTGCTTGTGCCCTGAAGGCTTACGGGCTGTACTGTGAGAGC
CAGATGGGGCAGGGGACACGCCAGCCCTACACCAGTCACGCCAGGCCACCGTCC
GACCCCTGGCATTGAGCCGTGAGCCCCACCTCCCTGCCGTGGGCTGCAGCGTACCTCC
AGGGGAGCTCGTGAGCTCAGGAGCCTCCGTCTCACCTATGCAACCTATGGGCC
AAGCGGCTGGTACGCTGCCACTGCCCTGCCCTCGCTGAGTACACGGTACCCAGCTGCG
GCCAACGCCACTTACTCCGTCTGTCTAGCCTTGGGCCGGGGCTGCCGGAGGGCG
AGGAGGCCTGCCGGGAGGCCATACACCCCCAGCCGTCCACTCCAACCACGCC
CAGGCCCGAGGGCAACCTGCCCTCATTGCCGCCCTGGCGCGGTGCTCCTGG
CGCGCTGGCTGCCGGTGGGGCAGCCTACTGTGTGCCGGGGGGCCATGGCAGCAGCG
CTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCCTGGAACTGGAGGGAGTGAAGGTC
CCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGGGCTGA
GTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGCCCTCCAGTCACCCCTCACGCAAAGC
CCTACATCTA**A**GGCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCGTGCCACACCAAGCTAAGTCTCAGTCCCAACCTGGGATGTGCGAGA
CAGGGCTGTGACCAAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGCACGGCGGGCCCTGCCATGTGCTGGTAAC
GCATGCCCTGGGCCCTGCTGGCTCTCCACTCCAGGGGACCCCTGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCAGGCTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTGGAAACATGTTTGCTTTAA
AATATATATATATTATAAGAGATCCTTCCCATTATTCTGGAAAGATGTTTCAAAC
AGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATGATGAAGGCCCTTGTAAAGAAAAA
ATAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, PI: 7.24, NX(S/T): 3

MCSRVPLLPPLLLALGPGVQGCPGQCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLLDSHNSLLALEPGIILDTANVEALRL
AGLGLQQLDEGLFSRLRNLDLSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSQLALPGDLSGLFPRLRLLAAARNPNCVCPPLSWFGPWVRESHVTLASP
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLTIGIEPVSPTRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV
TLRLPASLAEYVTQLRPNATYSVCVMPPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAVCVRRGRAMAAAQDKGQVPGAGPLELEGVKVPLEP
GPKATEGGEALPSGSECEVPLMGFPGPGLQSPFHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTCCCTCTGCACCACTGCCGTACCCCTACCGCCCCGCCACC
TCCTTGCTACCCACTCTGAAACCACAGCTGTTGCAGGGTCCCCAGCTC**ATGCCAGCCTC**
ATCTCCTTCTTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTGGTTGAGTTGGGGCAGCTCTGGGGCCGGCTTGCTG
ATGGCTCTGCTGACCCAAACACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGAGAATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAACAGCAGCACTCTGCTGCACCTGGTCCCATTAAACGCCACCTCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTAGGCGTGGAGAGGCCTAC
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTAGCCAGGTC
CTGTTCAAGACGTGACTTCACCATGGGTCAAGGTGGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCAGGCTACAAACAGCT
GCTATAGCGCAGGTGTCTCCATTACACCAAGGGATATTCTGAGTGTCTAAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTCCTGGGTTGTGAAACT**TGATT**
GTGTTATAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGGTACATACTGGAGACGCCAA
GAGCTGAGTATATAAGGAGAGGAAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC
CCCGTTCCCTCACTTTCCCTTTCAATTCCCACCCCTAGACTTGTGATTTACGGATATCTG
CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFILLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEYPWQSLPEQSSDALEAWENGERSRKRAVLTQKQKKQHSQLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTCTCCCTCTTCCCTTACTTCACTGGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGGGTGGGGGACCTGTGGCTCGTA
CCGCCCCCCCACCCCTCTTCACTGCCGTCTCCGGAAGACCTTCCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATGCCCGGACCTGGCCGGAGGAGGCTTGGCCGGGGAGA
TGCTCTAGGGCGGGCGGGAGGAGCGGCCGGGACGGAGGGCCGGAGGAAGATGGGC
TCCCCTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTGCCTTGCCTCTGGCCTGGT
CCTGAGTCGTGTGCCCATGTCCAGGGGAACAGCAGGAGTGGAGGGACTGAGGAGCTGC
CGTCGCCCTCCGGACCATGCCGAGAGGGCTGAAGAACACATGAAAAAATACAGGCCAGTCAG
GACCAGGGCTCCCTGCTTCCGGTCTGCGCTGCTGTGACCCGGTACCTCCATGTACCC
GGCGACCGCCGTGCCAGATCAACATCACTATCTGAAAGGGAGAAGGGTACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGCCAGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGCCCTGGGAGCGGTGCAAGAGCCACTACGCCG
CTTTTCGGTGGCCGGAAGAAGCCCAGTCACAGCAACCACTACTACAGACGGTATCTCG
ACACGGAGTTCGTGAACCTCTACGACCACTCAACATGTTCACCGGCAAGTTCTACTGCTAC
GTGCCCGCCTCTACTTCTCAGCCTCAACGTGACACCTGGAACCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTATCTGTTCGCGAGGTGGGACCCGAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACAGGTGGTACGCC
TACAAGGGCAGACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACCTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCACCTCCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTCCCCGATCCCTGGACTCCGACTC
CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAGGGATCGTGCTCC
CAGATCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGGGGACCCGC
GAGAACCCCTGGGACCTTCCCGGCCCTCTGCACACATCCTCAAGTGACCCGCACGGC
GAGACGGGGTGGCGCAGGGCGTCCAGGGTGGCACCAGGGCTCCAGTCCTGGAAATA
ATTAGGCAAATTCTAAAGGTCTCAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTGTCTTCCAGCCAGCCTGCTGGCTCCAAGAGAGAGGCCTTCAAGTGAG
ACTCTGCTTAAGAGAACGATCCAAAGTTAAAGCTCTGGGTGAGGGAGGGCCGGGGCAGG
AAACTACCTCTGGCTTAATTCTTTAAGCCACGTAGGAACCTTCTGAGGGATAGGTGGAC
CTGACATCCCTGTGGCCTTGGCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCAGGGT
GATGGGGCTGGGCCCCAGGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCC
TCCAGGGTGGTAGAACGAGCCGAAGGGCTCTGACAGTGGCCAGGGACCCCTGGTCCCCA
GGCCTGCAGATGTTCTATGAGGGGCAGAGCTCCTGGTACATCCATGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGGCCCTGGGGGTGGTCTCATGCCACCCCTGGCATCGGCT
TTCTGTGCCGCCTCCCACACAAATCAGCCCCAGAAGGCCCGGGCCTGGCTTGT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGCTAACCATCAGCGCTT
CCACGTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTGGACTGCC
CATCCAGGCCTCTGACCACTGAGGCTTCTAGGCTTCAAGCAGGGAGAG
CTGGAAGGGCTAGAAAGCTCCGCTTGTCTGTTCTCAGGCTCTGTGAGCCTCAGCCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCAATCACCGTGTAGGATTCACTCTCAGGAGC
TGGGTGGCAGGAGAGGAATAGCCCTGTGGCAATTGCAGGACAGCTGGAGCAGGGTGG
GTGTCTCCACGGTGTCTGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTTGCTACCCG
GCCAACCCCCGCTGCCCTCTTCCCTCCCCCATCCCCCACCTGGTTTGACTAAC
TCCCTCTGGGCTGGCTGCCGGACTGGGTCTAACGTCCTCTCTTAAAGAAACT
CTGCGGGTCAAGACTCTGAAGCCGAGTTGCTGTGGCGTCCCCGGAAGCAGAGGCC
GCTGCTTAAGCTCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVLFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GC GGAGCATCCGCTGCCGCTCTGCCGAGACCCCCGCCGGATTGCCGGCTTCCCGCG
GCGCAGAGCTGCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCTGACGCCA
GAGAGAAATCTCATCTGTGCAGCCTCTAAAGCAAACATAAGACCAAGGGAGGATTAT
CCTTGACCTTGAAGACCAAAACTAAACTGAAATTAAAATGTTCTTCGGGGAGAAGGGAG
CTTGACTTACACTTGTAAATAATTGCTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
AGAGGCAATGAGCCGTATATACTCAACTCAAGAAGACTGCATTAATTCTGCTGTTCAAC
AAAAAACATATCAGGGACAAAGCATGTAATTGATGATCTCGACACTCGAAAAACAGCTA
GACAACCCAACTGCTACCTATTCTGTCCCACGAGGAAGCCTGTCCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGACCAGAAATTGCCAAG
CCAAGAGTTACCCCAGGAAGATTCTCTTACATGGCAATTTCACAAGCAGTCACCCCC
TAGCCCACATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCA
GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTACAATTTCCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAAGCCGCCACCCCTCTACCCACCAATGCTTCAGTGACACC
TTCTGGGACTTCCCAGGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACACTGCACTTCTC
AGCCTCCCACGACCCCTCATTTCTACAGTTTACACGGGCTCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATACCCTTACAGAAATCTCAAACCTAAACTTGAACACAGGAAATGTGTATAACCTA
CTGCACCTTCTATGTCAAATGTGGAGTCTCCACTATGAATAAAACTGCTTCTGGAGGTT
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC
ATTGAAAAATGGCTTCTATCGGGCTCTGCTTTGGTGTCTGTTCTGGTGTAGGCC
TCGTCTCCTGGTAGAAATCCTTCGGAATCACTCCGCAAGAACGTTACTCAAGACTGGAT
TATTGATCAATGGGACTATGTGGACATTAAGGATGGAACTCGGTGTCCTTAATTCTT
TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTGCTAGTCTTAGCAGGAGGTTG
TATTGAAAGACAGGAAATGCCCTCTGCTTTCTTGTAGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCAGATCTGGCTCTCACCGCAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCTGCCTCAGCCTCTAAGTATCTGGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTGGTAGTTTAGTAGAGACGGGTTCACCATGTTGGTCAGGCTG
GTCTCAAACCTGTGACCTAGTGATCCACCCCTCTGGCTCCAAAGTGCTGGATTACAGG
CATGAGCCACACAGCTGGCCCCCTCTGTTATGTTGGTTTGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAATTGGTAATCTGTCTCTAAATATTAGCTAAAACAAAGCTCT
ATGTAAGTAATAAGTATAATTGCCATATAAAATTCAAACACTGGCTTTATGCAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCAATTGCTCACATTCTGGTTCCAGATAAAATCAAC
TGTTATATCAATTCTAATGGATTGCTTTCTTTATATGGATTCTTAAAACATTATT
CCAGATGTAGTTCTTCCAATTAAATATTGAATAAAATCTTTGTTACTCAA

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKSLEDVVIDIQSSLKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPPTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYILINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GGGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGGTGGTCTTC
GCCTCCTTGTGTGCCCTGGTATTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCCTATAGCATCCGCAGCAGCTGGGAGAGGCCTGCTCAAAGCTCCAGTCC
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAAATGTAACTGGGA
ATGTGACAGCAACACGATTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAAGAGTGCTGCTCCAAATCCCTGCTCTTATGGTACCTATGACGACGGAAAGCAC
AAGACTGAATAACGATGCCAAGAACATGCCATAGAACGACTTGGAAAGTAAAGAAATCAGGAACA
TGAAATTCAAGGTCTAGCTGGTATTTATTGCAGCAAAAGGCTGGAACTCCCTCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAACGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGCCTGAGTAAAT
GTGTTCTGTATAACAAATGCAGCTGGAATCGCTCAAGAACATCTTATTTCTAAATCCAACA
GCCCATTTGATGAGTATGGTTGTAAACCAATGAACATTGCTAGTTGTATCA
AATCTGGTACGCAGTATTTATACCAAGTATTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAA

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMDYEGDNGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125